

Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn  
 Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser  
 Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val  
 Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile  
 5 Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn  
 Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln  
 Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp  
 Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp  
 Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn  
 10 Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val  
 Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys  
 Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu  
 Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro  
 Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp  
 15 Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu  
 Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys  
 Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp  
 Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn  
 Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile  
 20 Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn  
 Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His  
 Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn  
 Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly  
 His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu  
 25 Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp  
 Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala  
 Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu  
 Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val  
 His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly  
 30 Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala  
 Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn  
 Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu  
 Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu  
 Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg  
 35 Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His  
 Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu  
 Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly  
 Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr  
 Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser  
 40 Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys  
 Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr  
 Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile  
 Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu  
 Leu Leu Met Glu Glu  
 45

## 5.14 EXAMPLE 14 -- NUCLEIC ACID SEQUENCES OF THE GENES

### ENCODING MODIFIED CRY1C\* CRYSTAL PROTEINS

#### 5.14.1 NUCLEIC ACID SEQUENCE OF *CRY1C-R148A* (SEQ ID NO:1)

5 ATGGAGGAAAATAATCAAAATCAATGCATACCTTACAATTGTTTAAGTAATCCTGAAGAAGTACTTTTGGAT  
GGAGAACGGATATCAACTGGTAATTCATCAATTGATATTTCTCTGTCACTTGTTTCTGGTATCTAAC  
10 TTTGTACCAGGGGGAGGATTTTGTAGTTGGATTAATAGATTTTGTATGGGGAATAGTTGGCCCTTCTCAATGG  
GATGCATTTCTAGTACAAATTGAACAATTAATTAATGAAAGAATAGCTGAATTTGCTAGGAATGCTGCTATT  
GCTAATTTAGAAAGGATTAGGAAACAATTTCAATATATATGTGGAAGCATTAAAGAATGGGAAGAAGATCCT  
AATAATCCAGCAACCAGGACCAGAGTAATTGATCGCTTTTCGTATACTTGATGGGCTACTTGAAAGGGACATT  
15 CCTTCGTTTGCAATTTCTGGATTTGAAGTACCCCTTTTATCCGTTTATGCTCAAGCGGCCAATCTGCATCTA  
GCTATATTAAGAGATTCTGTAATTTTGGAGAAAAGATGGGGATTGACAACGATAAATGTCAATGAAAACAT  
AATAGACTAATTAGGCATATTGATGAATATGCTGATCACTGTGCAAATACGTATAATCGGGGATTAAATAAT  
TTACCGAAATCTACGTATCAAGATTGGATAACATATAATCGATTACGGAGAGACTTAACTTGACTGTATTA  
GATATCGCCGCTTTCTTTCCAACTATGACAAATAGGAGATATCCAATTCAGCCAGTTGGTCAACTAACAGG  
20 GAAGTTTATACGGACCCATTAATTAATTTTAATCCACAGTTACAGTCTGTAGCTCAATTACCTACTTTTAAC  
GTTATGGAGAGCAGCGCAATTAGAAATCCTCATTATTTGATATATTGAATAATCTTACAATCTTTACGGAT  
TGGTTTAGTGTTGGACGCAATTTTATTGGGGAGGACATCGAGTAATATCTAGCCCTTATAGGAGGTGGTAAC  
ATAACATCTCCTATATATGGAAGAGAGGCGAACCAGGAGCCTCCAAGATCCTTTACTTTTAATGGACCGGTA  
TTTAGGACTTTATCAAATCCTACTTTACGATTATTACAGCAACCTTGGCCAGCGCCACCATTAAATTTACGT  
25 GGTGTTGAAGGAGTAGAATTTTCTACACCTACAAATAGCTTTACGTATCGAGGAAGAGGTACGGTTGATTCT  
TTAACTGAATTACCGCTGAGGATAATAGTGTGCCACCTCGCGAAGGATATAGTCATCGTTTATGTCATGCA  
ACTTTTGTCAAAGATCTGGAACACCTTTTAAACAACCTGGTGTAGTATTTTCTTGGACGCATCGTAGTGCA  
ACTCTTACAAATACAATTGATCCAGAGAGAATTAATCAAATACCTTTAGTGAAGGATTTAGAGTTTGGGGG  
GGCACCTCTGTCTATTACAGGACCAGGATTTACAGGAGGGGATATCCTTCGAAGAAATACCTTTGGTGATTTT  
30 GTATCTCTACAAGTCAATATTAATTCACCAATTACCCAAAGATACCGTTTAAAGATTTTCGTTACGCTTCCAGT  
AGGGATGCACGAGTTATAGTATTAACAGGAGCGGCATCCACAGGAGTGGGAGGCCAAGTTAGTGTAATATG  
CCTCTTCAGAAAATATGGAATAGGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTTAGTAAT  
CCTTTTTCATTTAGAGCTAATCCAGATATAATTGGGATAAGTGAACAACCTCTATTTGGTGCAGGTTCTATT  
AGTAGCGGTGAACCTTTATATAGATAAAATTGAAATTATTCTAGCAGATGCAACATTTGAAGCAGAATCTGAT  
35 TTAGAAAGAGCACAAAAGGCGGTGAATGCCCTGTTTACTTCTTCCAATCAAATCGGGTTAAAAACCGATGTG  
ACGGATTATCATATTGATCAAGTATCCAATTTAGTGGATTGTTTATCAGATGAATTTTGTCTGGATGAAAAG  
CGAGAATTGTCCGAGAAAGTCAAACATGCGAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCAAAC  
TTCAGAGGGATCAATAGACAACCAGACCGTGGCTGGAGAGGAAGTACAGATATTACCATCCAAGGAGGAGAT  
GACGTATTCAAAGAGAATTACGTCACACTACCGGTACCGTTGATGAGTGCTATCCAACGTATTTATATCAG  
40 AAAATAGATGAGTCGAAATTAAGCTTATACCCGTTATGAATTAAGAGGGTATATCGAAGATAGTCAAGAC  
TTAGAAATCTATTTGATCCGTTACAATGCAAAACACGAAATAGTAAATGTGCCAGGCACGGGTTCTTATGG  
CCGCTTTCAGCCCAAAGTCCAATCGGAAAGTGTGGAGAACCGAATCGATGCGCGCCACACCTTGAATGGAAT  
CCTGATCTAGATTGTTCTGTCAGAGACGGGGAAAAATGTGCACATCATTCCCATCATTTTACCTTGGATATT  
GATGTTGGATGTACAGACTTAAATGAGGACTTAGGTGTATGGGTGATATTCAAGATTAAGACGCAAGATGGC  
45 CATGCAAGACTAGGGAATCTAGAGTTTCTCGAAGAGAAAACATTATTAGGGGAAGCACTAGCTCGTGTGAAA  
AGAGCGGAGAAGAAGTGGAGAGACAAACGAGAGAAAACGAGTTGGAAACAAATATTGTTTATAAAGAGGCA  
AAAGAATCTGTAGATGCTTTATTTGTAACTCTCAATATGATAGATTACAAGTGGATACGAACATCGCAATG  
ATTCATGCGGCAGATAAACGCGTTTATAGAATCCGGGAAGCGTATCTGCCAGAGTTGTCTGTGATTCCAGGT  
GTCAATGCGGCCATTTTTCGAAGAATTAGAGGGACGTATTTTACAGCGTATTCTTATATGATGCGAGAAAT  
50 GTCATTAAAAATGGCGATTTCAATAATGGCTTATTATGCTGGAACGTGAAAGGTGATGTAGATGTAGAAGAG  
CAAAACAACCACCGTTTCGGTCTTGTATCCAGAATGGGAGGCAGAAGTGTCAAGAGGTTCTGTCTGT  
CCAGGTGCTGGCTATATCCTTCGTGTACAGCATATAAAGAGGGATATGGAGAGGGCTGCGTAACGATCCAT  
GAGATCGAAGACAATACAGACGAACGAAATTCAGCAACTGTGTAGAAGAGGAAGTATATCCAAACAACACA  
GTAACGTGTAATAATTATACTGGGACTCAAGAAGAATATGAGGGTACGTACACTTCTCGTAATCAAGGATAT  
GACGAAGCCTATGGTAATAACCTTCCGTACCAGCTGATTACGCTTCAGTCTATGAAGAAAAATCGTATACA  
GATGGACGAAGAGAGAATCCTTGTGAATCTAACAGAGGCTATGGGGATTACACACCACTACCGGCTGGTTAT

GTAACAAAGGATTTAGAGTACTTCCCAGAGACCGATAAGGTATGGATTGAGATCGGAGAAACAGAAGGAACA  
TTCATCGTGGATAGCGTGAATTACTCCTTATGGAGGAA

### 5.14.2 NUCLEIC ACID SEQUENCE OF *CRY1C-R148D* (SEQ ID NO:3)

5 ATGGAGGAAAATAATCAAAATCAATGCATACCTTACAATTGTTTAAAGTAATCCTGAAGAAGTACTTTTGGAT  
GGAGAACGGATATCAACTGGTAATTCATCAATTGATATTTCTCTGTCACTTGTTTCAGTTTCTGGTATCTAAC  
TTTGTACCAGGGGGAGGATTTTGTAGTTGGATTAATAGATTTTGTATGGGAATAGTTGGCCCTTCTCAATGG  
GATGCATTTCTAGTACAAATTGAACAATTAATTAATGAAAGAATAGCTGAATTTGCTAGGAATGCTGCTATT  
10 GCTAATTTAGAAGGATTAGGAAACAATTTCAATATATATGTGGAAGCATTAAAGAATGGGAAGAAGATCCT  
AATAATCCAGCAACCAGGACCAGAGTAATTGATCGCTTTCGTATACTTGATGGGCTACTTGAAAGGGACATT  
CCTTCGTTTGACATTTCTGGATTTGAAGTACCCCTTTTATCCGTTTATGCTCAAGCGGCCAATCTGCATCTA  
GCTATATTAAGAGATTCTGTAATTTTGGAGAAAGATGGGGATTGACAACGATAAATGTCAATGAAAACCTAT  
AATAGACTAATTAGGCATATTGATGAATATGCTGATCACTGTGCAAATACGTATAATCGGGGATTAAATAAT  
TTACCGAAATCTACGTATCAAGATTGGATAACATATAATCGATTACGGAGAGACTTAACATTGACTGTATTA  
15 GATATCGCCGCTTTCTTTCCAAACTATGACAATAGGAGATATCCAATTACGCCAGTTGGTCAACTAACAAGG  
GAAGTTTATACGGACCCATTAAATTAATTTTAAATCCACAGTTACAGTCTGTAGCTCAATTACCTACTTTTAAAC  
GTTATGGAGAGCAGCGCAATTAGAAATCCTCATTTATTTGATATATTGAATAATCTTACAATCTTTACGGAT  
TGGTTTGTAGTGTGGACGCAATTTTATTGGGGAGGACATCGAGTAATATCTAGCCTTATAGGAGGTGGTAAC  
ATAACATCTCCTATATATGGAAGAGAGGCGAACCAGGAGCCTCCAAGATCCTTTACTTTTAAATGGACCGGTA  
20 TTTAGGACTTTATCAAATCCTACTTTACGATTATTACAGCAACCTTGGCCAGCGCCACCATTAAATTTACGT  
GGTGTGGAAGGAGTAGAATTTTCTACACCTACAAATAGCTTTACGTATCGAGGAAGAGGTACGGTTGATTCT  
TTAACTGAATTACCGCCTGAGGATAATAGTGTGCCACCTCGCGAAGGATATAGTCATCGTTTATGTCATGCA  
ACTTTTGTTCAAAGATCTGGAACACCTTTTTTAACTGGTGTAGTATTTTCTTGGACGCATCGTAGTGCA  
ACTCTTACAAATACAATTGATCCAGAGAGAATTAATCAAATACCTTTAGTGAAAGGATTTAGAGTTTGGGGG  
25 GGCACCTCTGTCATTACAGGACCAGGATTTACAGGAGGGGATATCCTTCGAAGAAATACCTTTGGTGATTTT  
GTATCTCTACAAGTCAATATTAATTCACCAATTACCCAAAGATACCGTTTAAAGATTTCTGTACGCTTCCAGT  
AGGGATGCACGAGTTATAGTATTAACAGGAGCGGCATCCACAGGAGTGGGAGGCCAAGTTAGTGTAATATG  
CCTCTTCAGAAAATATGGAAATAGGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTTAGTAAT  
CCTTTTTTCATTTAGAGCTAATCCAGATATAATTGGGATAAGTGAACAACCTCTATTTGGTGCAGGTTCTATT  
30 AGTAGCGGTGAACCTTTATATAGATAAAATTGAAATTATTCTAGCAGATGCAACATTTGAAGCAGAATCTGAT  
TTAGAAAGAGCACAAAAGGCGGTGAATGCCCTGTTTACTTCTTCCAATCAAATCGGGTTAAAAACCGATGTG  
ACGGATTATCATATTGATCAAGTATCCAATTTAGTGGATTGTTTATCAGATGAATTTTGTCTGGATGAAAAG  
CGAGAATTGTCCGAGAAAGTCAAACATGCGAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCAAAC  
TTCAGAGGGATCAATAGACAACCAGACCGTGGCTGGAGAGGAAGTACAGATATTACCATCCAAGGAGGAGAT  
35 GACGTATTCAAAGAGAATTACGTACACTACCGGGTACCGTTGATGAGTGCTATCCAACGTATTTATATCAG  
AAAATAGATGAGTCGAAATTAAGGCTTATACCCGTTATGAATTAAGAGGGTATATCGAAGATAGTCAAGAC  
TTAGAAATCTATTTGATCCGTTACAATGCAAAACACGAAATAGTAAATGTGCCAGGCACGGGTTCTTTATGG  
CCGCTTTCAGCCCAAAGTCCAATCGGAAAGTGTGGAGAACCGAATCGATGCGCGCCACACCTTGAATGGAAT  
CCTGATCTAGATTGTTCTGCAGAGACGGGGAAAAATGTGCACATCATTCCCATCATTTACCTTGGATATT  
40 GATGTTGGATGTACAGACTTAAATGAGGACTTAGGTGTATGGGTGATATTCAAGATTAAGACGCAAGATGGC  
CATGCAAGACTAGGGAATCTAGAGTTTCTCGAAGAGAAACCATTATTAGGGGAAGCACTAGCTCGTGTGAAA  
AGAGCGGAGAAGAAGTGGAGAGACAAACGAGAGAACTGCAGTTGGAAACAAATATTGTTTATAAAGAGGCA  
AAAGAATCTGTAGATGCTTTATTTGTAACTCTCAATATGATAGATTACAAGTGGATACGAACATCGCAATG  
ATTCATGCGGCAGATAAACCGGTTTATAGAATCCGGGAAGCGTATCTGCCAGAGTTGTCTGTGATTCCAGGT  
45 GTCAATGCGGCCATTTTTCGAAGAATTAGAGGGACGTATTTTACAGCGTATTCCTTATATGATGCGAGAAAT  
GTCATTAAAAATGGCGATTTCAATAATGGCTTATTATGCTGGAACGTGAAAGGTCATGTAGATGTAGAAGAG  
CAAAACAACCACCGTTCGGTCTTGTATCCCAGAATGGGAGGCAGAAGTGTACAAGAGGTTCTGTGTCTGT  
CCAGGTCTGTGGCTATATCCTTCGTGTACAGCATATAAAGAGGGATATGGAGAGGGCTGCGTAACGATCCAT  
GAGATCGAAGACAATACAGACGAACTGAAATTCAGCAACTGTGTAGAAGAGGAAGTATATCCAAACAACACA  
50 GTAACGTGTAATAATTATACTGGGACTCAAGAAGAATATGAGGGTACGTACACTTCTCGTAATCAAGGATAT  
GACGAAGCCTATGGTAATAACCCCTTCGTACCAGCTGATTACGCTTCAGTCTATGAAGAAAAATCGTATACA  
GATGGACGAAGAGAGAATCCTTGTGAATCTAACAGAGGCTATGGGGATTACACACCACTACCGGCTGGTTAT